

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/818,990

DATE: 10/11/2001

TIME: 10:40:51

Input Set : A:\LEX-0152-USA SEQLIST.txt

Output Set: N:\CRF3\10112001\I818990.raw

4 <110> APPLICANT: Walke, D. Wade
5 Donoho, Gregory
6 Scoville, John
7 Hilbun, Erin,
8 Zambrowicz, Brian
9 Turner, C. Alexander Jr.
11 <120> TITLE OF INVENTION: Novel Human Proteins and Polynucleotides Encoding the Same
13 <130> FILE REFERENCE: LEX-0152-USA
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/818,990
C--> 15 <141> CURRENT FILING DATE: 2001-03-27
15 <150> PRIOR APPLICATION NUMBER: US 60/192,218
16 <151> PRIOR FILING DATE: 2000-03-27
18 <160> NUMBER OF SEQ ID NOS: 31
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3963
24 <212> TYPE: DNA
25 <213> ORGANISM: homo sapiens
27 <400> SEQUENCE: 1

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29 ttagctgaaa ccagacatcg gggaaacaat gagaggagtc ggcggagcc ctcctccaac	120
30 ccttgccatt tcggcagtc ttctggggcc gctgaaggag gcggaggcca agatgacctt	180
31 ccagatcttt cagcctttct gagccaagaa gaattagacg aaagtgtcaa tttggcaaga	240
32 ctggccatca attacgaccc tttggagaag gcagatgaaa ctcaagctag aaaacgactt	300
33 tctcctgatc agatgaaaca ctcacctaata ttaagttttg agcctaactt ctgccaggat	360
34 aaccctcgaa gtcccaccag ctctaaagaa agccccagg aggcacaaaag gccacagtat	420
35 tgttctgaaa ccagtcctaa aaaagtattt ttaaataagg ctgccgactt cattgaagag	480
36 ctatcctccc ttttcaaatc ccacagctcc aaaaggatta gacctcgtgc ctgcaaaaac	540
37 cacaagagta aactggaatc tcaaaaacaaa gttatgcagg aaaacagctc cagttttctca	600
38 gatctgtcag aaagacgaga aagatcttct gtccccatcc ctatccctgc ggataccagg	660
39 gataatgaag tgaatcacgc cctggaacag caggaagcca agaggcgtga agcggagcag	720
40 gctgccagtg aggcggctgg tggagacact acaccagggt cttccccttc atctctgtac	780
41 tatgaagaac ctctggggca acctccccgg ttactcaaaa agttacggag cagagaagtt	840
42 ccagaaggaa ctcgagtaca gttggattgc atagtggtag gaattccacc acctcaagta	900
43 agtggttact gtgaaggcaa ggagcttgaa aattccccag atattcacat cgtccaggca	960
44 ggaaatctgc actcactgac cattgcggaa gcctttgaag aggacacagg acgctattcc	1020
45 tgctttgctt ctaacatcta tgggacagat tcgacttctg ctgagattta tatagaaggg	1080
46 gtttcttctt ctgactcaga aggcgacctt aacaaggaag agatgaatcg aatccagaag	1140
47 ccaaatgagg tgtcatctcc tcccactacc tctgcagtca ttcctccagc agtaccctaa	1200
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49 aattacttgc agggattgga tggaaaacct atcattgcag ctctgtgtgt tacaagatg	1320
50 ctacaaaatt tgtcagcttc tgagggtcag ctggtgtgtt ttgaatgcag agtaaaagga	1380
51 gctccatctc ctaaggttga gtggtataga gaagggactt taatagaaga ttctccagat	1440
52 tttaggattt tacagaaaaa acctcgatcc atggcagagc cagaggagat ttgcacctg	1500
53 gtcattgctg aggtgtttgc agaagattct ggggtgcttca catgtactgc aagcaacaaa	1560
54 tacggcacag tgtcaagcat tgcacagctg cacgtgagag gaaatgagga cctcagcaac	1620
55 aacgggtctc ttcactcagc caactcyacc accaacctgg cagctattga gccacagccc	1680

ENTERED

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56 tccccacccc actcagagcc tccatctgtg gaacaacccc ccaaacccaa actcgagggg 1740
57 gttctggtga accacaatga gccccggtcc agctccagga ttgggcttcg tgtgcacttc 1800
58 aacctgcctg aagatgacaa aggaagtga gcatcctccg aggctggtgt ggtgaccacc 1860
59 agacagacca ggcccgatcc tttscaggag aggttcaacg gacaggcaac aaaaacccca 1920
60 gagccttctt tccccgtgaa agagccccct ccagttcttg ccaaacccaa acttgattcc 1980
61 actcagttac aacagcttca taaccaagtc ttactggaac aacaccaatt gcaaaaccca 2040
62 cctccttcat ctctaagga gtttctttc arcattgactg ttttgaactc caatgctccc 2100
63 ccagcggtag caacatccar taagcaggtg aaggctcctt catcacagac gttcagcttg 2160
64 gcccggccga agtatttctt cccctccacg aacaccaccg cagcaactgt ggccccttcc 2220
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66 gaaagcctct tagtgtctca cccctctgtg caaaccaaa ttcagaggag gctttccatc 2340
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68 atccccagcg gaaaccagtt tcagccccgc tgtgtgtccc caattcctgt ctctcctacc 2460
69 agccggattc agaaccaggt ggctttctc agctctgttc tgccttctct ccctgccatc 2520
70 ccaccacaaa atgccatggr gctgcctaga agtgcaccat ccatgccatc ccagggatta 2580
71 gcgaagaaaa atacaaagtc tcctcaacca gtgaatgatg ataacattcg tgaaactaag 2640
72 aacgcagtga ttcgagactt ggggaaaaaa ataactttca gtgatgtcag accaaaccag 2700
73 caggagtaca aaatttcaag ctttgagcag aggtgatga atgaaataga gtttcgcttg 2760
74 gaacgtactc ctgttgatga atcagatgat gaaattcaac atgatgagat cccacgggc 2820
75 aagtgtattg ctcccatctt tgacaagaga ctcaagcact tccgggtcac agaaggctct 2880
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77 gatgggaagc agatttctaa gagaaatgag cactgcaaaa tgaggcgaga aggagatggg 3000
78 acatgctctc tgcacattga atccactacc agtgatgacg atggcaacta caccatcatg 3060
79 gcagccaacc ccagggggag aatcagctgt tctggccact tgatggtaca aagtttgccc 3120
80 attcgagtc ggctaaccct tgctggtcag tctcacaggg gaagatcccg agtgcaagaa 3180
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83 cccccggagc tgacatggct actcaatggc caacctgtgc taccagatgc ctcccacaag 3360
84 atgctggtca gggagaccgg agtccactct ctgctcattg acccactcac tcagcgcgac 3420
85 gcagggacct ataagtgcac cgctaccaac aaaaccgggc agaattcttt tagtctggag 3480
86 ctctctgtag tagccaaaga ggtgaagaaa gcacctgtga tcttgagaa actacagaac 3540
87 tgcggtgttc ccgaaggcca ccccgtaga ctggagtgc gcgtgatagg catgccccca 3600
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90 gctggatggt acacgtgtc agccaagaat gaagccggca tctgtctgtg cactgccagg 3780
91 ctggatatat acgctcagtg gcaccatcag atcccaccgc ccatgtctgt ccggcccagt 3840
92 ggcagtcgct acggtctctt caccagtaaa ggacttgaca tattttctgc cttttcctcc 3900
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94 taa 3963

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96 <210> SEQ ID NO: 2

97 <211> LENGTH: 1320

98 <212> TYPE: PRT

99 <213> ORGANISM: homo sapiens

101 <220> FEATURE:

102 <221> NAME/KEY: VARIANT

103 <222> LOCATION: (1)...(1320)

104 <223> OTHER INFORMATION: Xaa = Any Amino Acid

106 <400> SEQUENCE: 2

107 Met Gln Asp Asp Ser Ile Glu Ala Ser Thr Ser Ile Ser Gln Leu Leu

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108 1          5          10          15
109 Arg Glu Ser Tyr Leu Ala Glu Thr Arg His Arg Gly Asn Asn Glu Arg
110          20          25          30
111 Ser Arg Ala Glu Pro Ser Ser Asn Pro Cys His Phe Gly Ser Pro Ser
112          35          40          45
113 Gly Ala Ala Glu Gly Gly Gly Gly Gln Asp Asp Leu Pro Asp Leu Ser
114          50          55          60
115 Ala Phe Leu Ser Gln Glu Glu Leu Asp Glu Ser Val Asn Leu Ala Arg
116 65          70          75          80
117 Leu Ala Ile Asn Tyr Asp Pro Leu Glu Lys Ala Asp Glu Thr Gln Ala
118          85          90          95
119 Arg Lys Arg Leu Ser Pro Asp Gln Met Lys His Ser Pro Asn Leu Ser
120          100          105          110
121 Phe Glu Pro Asn Phe Cys Gln Asp Asn Pro Arg Ser Pro Thr Ser Ser
122          115          120          125
123 Lys Glu Ser Pro Gln Glu Ala Lys Arg Pro Gln Tyr Cys Ser Glu Thr
124          130          135          140
125 Gln Ser Lys Lys Val Phe Leu Asn Lys Ala Ala Asp Phe Ile Glu Glu
126 145          150          155          160
127 Leu Ser Ser Leu Phe Lys Ser His Ser Ser Lys Arg Ile Arg Pro Arg
128          165          170          175
129 Ala Cys Lys Asn His Lys Ser Lys Leu Glu Ser Gln Asn Lys Val Met
130          180          185          190
131 Gln Glu Asn Ser Ser Ser Phe Ser Asp Leu Ser Glu Arg Arg Glu Arg
132          195          200          205
133 Ser Ser Val Pro Ile Pro Ile Pro Ala Asp Thr Arg Asp Asn Glu Val
134          210          215          220
135 Asn His Ala Leu Glu Gln Gln Glu Ala Lys Arg Arg Glu Ala Glu Gln
136 225          230          235          240
137 Ala Ala Ser Glu Ala Ala Gly Gly Asp Thr Thr Pro Gly Ser Ser Pro
138          245          250          255
139 Ser Ser Leu Tyr Tyr Glu Glu Pro Leu Gly Gln Pro Pro Arg Phe Thr
140          260          265          270
141 Gln Lys Leu Arg Ser Arg Glu Val Pro Glu Gly Thr Arg Val Gln Leu
142          275          280          285
143 Asp Cys Ile Val Val Gly Ile Pro Pro Pro Gln Val Arg Trp Tyr Cys
144          290          295          300
145 Glu Gly Lys Glu Leu Glu Asn Ser Pro Asp Ile His Ile Val Gln Ala
146 305          310          315          320
147 Gly Asn Leu His Ser Leu Thr Ile Ala Glu Ala Phe Glu Glu Asp Thr
148          325          330          335
149 Gly Arg Tyr Ser Cys Phe Ala Ser Asn Ile Tyr Gly Thr Asp Ser Thr
150          340          345          350
151 Ser Ala Glu Ile Tyr Ile Glu Gly Val Ser Ser Ser Asp Ser Glu Gly
152          355          360          365
153 Asp Pro Asn Lys Glu Glu Met Asn Arg Ile Gln Lys Pro Asn Glu Val
154          370          375          380
155 Ser Ser Pro Pro Thr Thr Ser Ala Val Ile Pro Pro Ala Val Pro Gln
156 385          390          395          400

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```

157 Ala Gln His Leu Val Ala Gln Pro Arg Val Ala Thr Ile Gln Gln Cys
158                               405                               410                               415
159 Gln Ser Pro Thr Asn Tyr Leu Gln Gly Leu Asp Gly Lys Pro Ile Ile
160                               420                               425                               430
161 Ala Ala Pro Val Phe Thr Lys Met Leu Gln Asn Leu Ser Ala Ser Glu
162                               435                               440                               445
163 Gly Gln Leu Val Val Phe Glu Cys Arg Val Lys Gly Ala Pro Ser Pro
164                               450                               455                               460
165 Lys Val Glu Trp Tyr Arg Glu Gly Thr Leu Ile Glu Asp Ser Pro Asp
166 465                               470                               475                               480
167 Phe Arg Ile Leu Gln Lys Lys Pro Arg Ser Met Ala Glu Pro Glu Glu
168                               485                               490                               495
169 Ile Cys Thr Leu Val Ile Ala Glu Val Phe Ala Glu Asp Ser Gly Cys
170                               500                               505                               510
171 Phe Thr Cys Thr Ala Ser Asn Lys Tyr Gly Thr Val Ser Ser Ile Ala
172                               515                               520                               525
173 Gln Leu His Val Arg Gly Asn Glu Asp Leu Ser Asn Asn Gly Ser Leu
174                               530                               535                               540
175 His Ser Ala Asn Ser Thr Thr Asn Leu Ala Ala Ile Glu Pro Gln Pro
176 545                               550                               555                               560
177 Ser Pro Pro His Ser Glu Pro Pro Ser Val Glu Gln Pro Pro Lys Pro
178                               565                               570                               575
179 Lys Leu Glu Gly Val Leu Val Asn His Asn Glu Pro Arg Ser Ser Ser
180                               580                               585                               590
181 Arg Ile Gly Leu Arg Val His Phe Asn Leu Pro Glu Asp Asp Lys Gly
182                               595                               600                               605
183 Ser Glu Ala Ser Ser Glu Ala Gly Val Val Thr Thr Arg Gln Thr Arg
184                               610                               615                               620
W--> 185 Pro Asp Ser Xaa Gln Glu Arg Phe Asn Gly Gln Ala Thr Lys Thr Pro
186 625                               630                               635                               640
187 Glu Pro Ser Phe Pro Val Lys Glu Pro Pro Pro Val Leu Ala Lys Pro
188                               645                               650                               655
189 Lys Leu Asp Ser Thr Gln Leu Gln Gln Leu His Asn Gln Val Leu Leu
190                               660                               665                               670
191 Glu Gln His Gln Leu Gln Asn Pro Pro Pro Ser Ser Pro Lys Glu Phe
192                               675                               680                               685
W--> 193 Pro Phe Xaa Met Thr Val Leu Asn Ser Asn Ala Pro Pro Ala Val Thr
194                               690                               695                               700
W--> 195 Thr Ser Xaa Lys Gln Val Lys Ala Pro Ser Ser Gln Thr Phe Ser Leu
196 705                               710                               715                               720
197 Ala Arg Pro Lys Tyr Phe Phe Pro Ser Thr Asn Thr Thr Ala Ala Thr
198                               725                               730                               735
199 Val Ala Pro Ser Ser Ser Pro Val Phe Thr Leu Ser Ser Thr Pro Gln
200                               740                               745                               750
201 Thr Ile Gln Arg Thr Val Ser Lys Glu Ser Leu Leu Val Ser His Pro
202                               755                               760                               765
203 Ser Val Gln Thr Lys Ser Pro Gly Gly Leu Ser Ile Gln Asn Glu Pro
204                               770                               775                               780
205 Leu Pro Pro Gly Pro Thr Glu Pro Thr Pro Pro Pro Phe Thr Phe Ser

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206 785 790 795 800
 207 Ile Pro Ser Gly Asn Gln Phe Gln Pro Arg Cys Val Ser Pro Ile Pro
 208 805 810 815
 209 Val Ser Pro Thr Ser Arg Ile Gln Asn Pro Val Ala Phe Leu Ser Ser
 210 820 825 830
 W--> 211 Val Leu Pro Ser Leu Pro Ala Ile Pro Pro Thr Asn Ala Met Xaa Leu
 212 835 840 845
 213 Pro Arg Ser Ala Pro Ser Met Pro Ser Gln Gly Leu Ala Lys Lys Asn
 214 850 855 860
 215 Thr Lys Ser Pro Gln Pro Val Asn Asp Asp Asn Ile Arg Glu Thr Lys
 216 865 870 875 880
 217 Asn Ala Val Ile Arg Asp Leu Gly Lys Lys Ile Thr Phe Ser Asp Val
 218 885 890 895
 219 Arg Pro Asn Gln Gln Glu Tyr Lys Ile Ser Ser Phe Glu Gln Arg Leu
 220 900 905 910
 221 Met Asn Glu Ile Glu Phe Arg Leu Glu Arg Thr Pro Val Asp Glu Ser
 222 915 920 925
 223 Asp Asp Glu Ile Gln His Asp Glu Ile Pro Thr Gly Lys Cys Ile Ala
 224 930 935 940
 225 Pro Ile Phe Asp Lys Arg Leu Lys His Phe Arg Val Thr Glu Gly Ser
 226 945 950 955 960
 227 Pro Val Thr Phe Thr Cys Lys Ile Val Gly Ile Pro Val Pro Lys Val
 228 965 970 975
 229 Tyr Trp Phe Lys Asp Gly Lys Gln Ile Ser Lys Arg Asn Glu His Cys
 230 980 985 990
 231 Lys Met Arg Arg Glu Gly Asp Gly Thr Cys Ser Leu His Ile Glu Ser
 232 995 1000 1005
 233 Thr Thr Ser Asp Asp Asp Gly Asn Tyr Thr Ile Met Ala Ala Asn Pro
 234 1010 1015 1020
 235 Gln Gly Arg Ile Ser Cys Ser Gly His Leu Met Val Gln Ser Leu Pro
 236 1025 1030 1035 1040
 237 Ile Arg Ser Arg Leu Thr Ser Ala Gly Gln Ser His Arg Gly Arg Ser
 238 1045 1050 1055
 239 Arg Val Gln Glu Arg Asp Lys Glu Pro Leu Gln Glu Arg Phe Phe Arg
 240 1060 1065 1070
 241 Pro His Phe Leu Gln Ala Pro Gly Asp Met Val Ala His Glu Gly Arg
 242 1075 1080 1085
 243 Leu Cys Arg Leu Asp Cys Lys Val Ser Gly Leu Pro Pro Glu Leu
 244 1090 1095 1100
 245 Thr Trp Leu Leu Asn Gly Gln Pro Val Leu Pro Asp Ala Ser His Lys
 246 1105 1110 1115 1120
 247 Met Leu Val Arg Glu Thr Gly Val His Ser Leu Leu Ile Asp Pro Leu
 248 1125 1130 1135
 249 Thr Gln Arg Asp Ala Gly Thr Tyr Lys Cys Ile Ala Thr Asn Lys Thr
 250 1140 1145 1150
 251 Gly Gln Asn Ser Phe Ser Leu Glu Leu Ser Val Val Ala Lys Glu Val
 252 1155 1160 1165
 253 Lys Lys Ala Pro Val Ile Leu Glu Lys Leu Gln Asn Cys Gly Val Pro
 254 1170 1175 1180

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

L:883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:1015 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:1017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:1410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28

L:1416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28

L:1418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28